REMARKS/ARGUMENTS

Claims 1, 4-11, 21-23, 26-29 and 31-35 are active. Claim 1 has been amended by substituting the text of prior claim 30 with the term "a) to j)" at the line after the table being revised to "a) to l)" for consistency with the table. This revision avoids introducing awkward dependencies into the claims dependent on claim 1, which imposing the limitations of claim 30 on those claims. Claim 34 tracks the allowable subject matter previously identified by the Examiner. New claims 34 and 35 cover the subject matter of claims 4 and 27 indicated as allowable in the final Official Action dated October 14, 2008. No new matter is believed to have been added. Favorable consideration of this amendment and allowance of the case are respectfully requested.

Lack of Unity/Restriction/Election

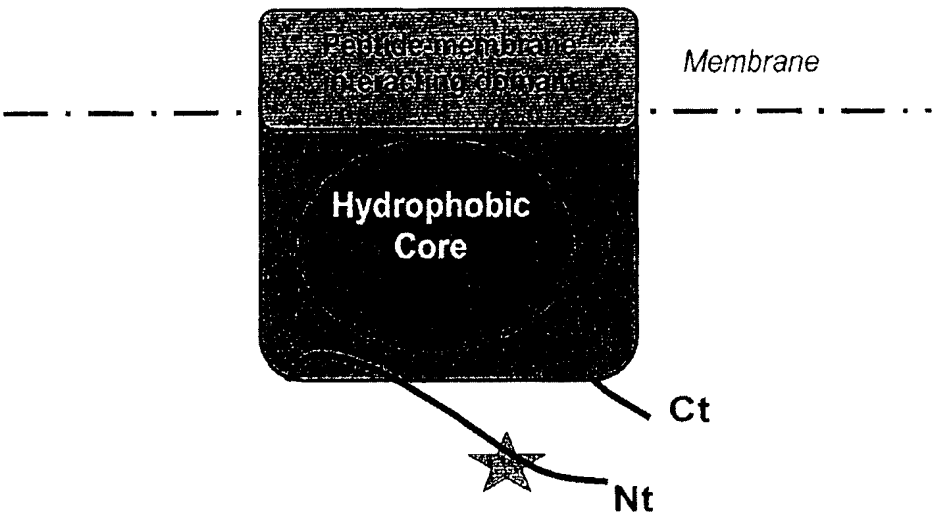
The Applicants previously elected with traverse Group I. This requirement has been made FINAL. The non-elected claims have been cancelled without prejudice.

Rejection—35 U.S.C. §112, first paragraph

Claims 1, 5-11, 21-23, 26-28 and 30-33 were rejected under 35 U.S.C. 112, first paragraph, as lacking adequate written description on the ground that no descriptive support was provided for particular selections of amino acid residues at positions like J1, etc. As shown in the attached Table A, the specification extensively exemplifies particular selections of amino acids required at the particular residues like J1. For example, J1 is G, N, D, P or H in SEQ ID NOS: 1, 2, 3, 7 and 8 as shown in the attached table, therefore, these selections are expressly described and exemplified for J1. Similarly, the other J residues, such as J26 are exemplified by the original disclosure as evident from Table A. Therefore, the Applicants

particular position "J" at the time this application was filed and no new matter has been introduced.

The polypeptides of the invention share a higher order secondary or tertiary structure. Selection of the particular amino acid choices at various J positions provide annexin-like peptides with improved properties in terms of affinity for phospholipids, toxicity, thermodynamic stability, and reversibility of their folding processes when compared to prior art peptides. This higher order structure comprises a hydrophobic core and a peptide membrane-interacting domain as depicted below.



As explained in paragraphs [076] and [0082] of U.S. 2006/0233706, the domain that directly or indirectly interacts with the membrane lipids mainly comprises the residues 12, 15, 16, 17, 19, 20, 22, 50, 55, 57, 58, 59, 60 and 65. These residues, which are identified by claim 1, affect the affinity of the peptide affinity for lipids.

The thermodynamic properties and stability of this peptide depends on the hydrophobic core residues of which are the residues U shown in Table 1. To improve the properties in comparison with annexin, the inventors chose particular combinations of hydrophobic residues.

As shown in the diagram above, various N- and C-terminal segments appear in the lower portion of the moleculeThe lower part of the peptide according to the invention includes, in particular, N-terminal ("Nt") and C-terminal ("Ct") segments can be used for for labeling or grafting the molecule onto a solid support.

The surface residues of the polypeptide can vary as described in claim 1. However, in general most selections share physiochemical properties as shown in the Venn diagram below.

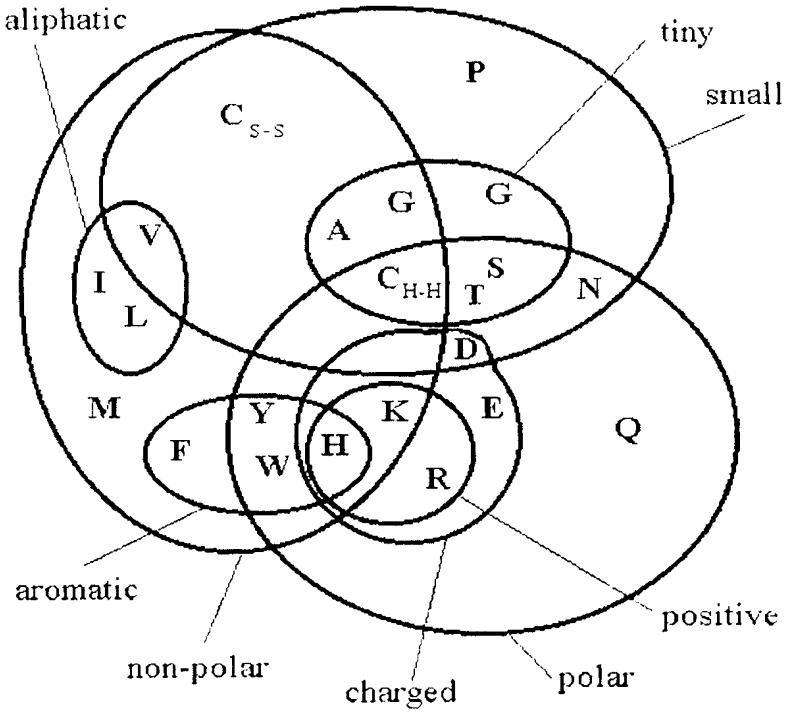


Figure 1. A Venn diagram showing the relationship of the 20 naturally occurring amino acids to a selection of physico-chemical properties thought to be important in the determination of protein structure (http://prowl.rockefeller.edu/aainfo/pchem.htm).

Accordingly, no new matter has been incorporated because each particular J selection is actually exemplified in the specification and the Applicants clearly possessed the identities of each particular J substitution and the concepts of the interchangability of the specified residues at a particular J position at the time of filing.

Rejection--35 U.S.C. §112, second paragraph

Claims 4 and 29-33 were rejected under 35 U.S.C. 112, second paragraph, as being indefinite. The numbering convention of the J residues as used in the specification differs from the numbering as it appears in the sequence listing. The sequence listing and the motifs depicted in PI differ due to sequence rule requirements that specify that the first residue in each sequence start with 1. To resolve this incongruity, the Applicants attach herewith a tabular concordance depicting the various "J" residues of (PI) in the context of each SEQ ID NO. As shown, all of the claimed sequences find antecedent basis in the independent claim. For example, residue J26 in SEQ ID NO: 11 is L (leu, leucine), which is also apparent from SEQ ID NO: 11 where positions 11, 16 and 18 correspond to residues 7 (Asp), 12 (Arg) and 14 (Ala) in(PI)(SEQ ID NO: 18). J26 in SEQ ID NOS: 12-14 is also L (leu, leucine). Similarly, J64 in SEQ ID NOS: 11-14 is F (Phe, phenylalanine) which conforms to the Markush grouping in independent claim 1. Accordingly, this rejection may now be withdrawn.

Conclusion

This application presents allowable subject matter and the Examiner is respectfully requested to pass it to issue. The Examiner is kindly invited to contact the undersigned should a further discussion of the issues or claims be helpful.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.
Norman F. Oblon

Thomas M. Cunningham
Registration No. 45,394

Customer Number
22850

Tel: (703) 413-3000
Fax: (703) 413 -2220
(OSMMN 08/07)